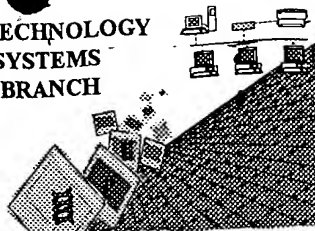


DeClark

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/857,097A
Source: 1600 RUSH
Date Processed by STIC: 9/19/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/857,097A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ✓ Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

DATE: 09/19/2002

PATENT APPLICATION: US/09/857,097A

TIME: 13:04:24

Input Set : A:\EP.txt

Output Set: N:\CRF4\09192002\I857097A.raw

4 <110> APPLICANT: Urbaniak, Stanislaw J.
 5 Barker, Robert N.
 7 <120> TITLE OF INVENTION: ALLO- AND AUTO-REACTIVE T-CELL EPITOPES
 9 <130> FILE REFERENCE: P097
 11 <140> CURRENT APPLICATION NUMBER: 09/857,097A
 12 <141> CURRENT FILING DATE: 1999-12-01
 14 <150> PRIOR APPLICATION NUMBER: 9826378.3
 15 <151> PRIOR FILING DATE: 1998-12-01
 E--> 17 <160> NUMBER OF SEQ ID NOS: 152 46 (p.6)
 19 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 15
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: RhCE (R2 cE) Residues 2-16
 29 <400> SEQUENCE: 1
 30 Ser Ser Lys Tyr Pro Arg Ser Val Arg Arg Cys Leu Pro Leu Trp
 E--> 31 1 + 5 5 10 10 15
 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 15
 37 <212> TYPE: PRT
 38 <213> ORGANISM: Homo sapiens
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: RhCE (R2 cE) Residues 12-26
 43 <400> SEQUENCE: 2
 44 Cys Leu Pro Leu Trp Ala Leu Thr Leu Glu Ala Ala Leu Ile Leu
 E--> 45 1 5 10 15
 46 <210> SEQ ID NO: 3
 49 <211> LENGTH: 15
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Homo sapiens
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 22-36
 56 <400> SEQUENCE: 3
 57 Ala Ala Leu Ile Leu Leu Phe Tyr Phe Phe Thr His Tyr Asp Ala
 E--> 58 1 5 10 15
 62 <210> SEQ ID NO: 4
 63 <211> LENGTH: 15

Does Not Comply
 Corrected Diskette Needed

pp 1-6

global error
 misaligned amino
 acid numbers
 (see
 item 3 on Error
 summary sheet)

same error

same

RAW SEQUENCE LISTING

DATE: 09/19/2002

PATENT APPLICATION: US/09/857,097A

TIME: 13:04:24

Input Set : A:\EP.txt

Output Set: N:\CRF4\09192002\I857097A.raw

64 <212> TYPE: PRT
65 <213> ORGANISM: Homo sapiens
67 <220> FEATURE:
68 <223> OTHER INFORMATION: RhCE (R2 cE) Residues 32-46
70 <400> SEQUENCE: 4
71 Thr His Tyr Asp Ala Ser Leu Glu Asp Gln Lys Gly Leu Val Ala
E--> 72 1 5 10 15
76 <210> SEQ ID NO: 5
77 <211> LENGTH: 15
78 <212> TYPE: PRT
79 <213> ORGANISM: Homo sapiens
81 <220> FEATURE:
82 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 42-56
84 <400> SEQUENCE: 5
85 Lys Gly Leu Val Ala Ser Tyr Gln Val Gly Gln Asp Leu Thr Val
E--> 86 1 5 10 15
89 <210> SEQ ID NO: 6
90 <211> LENGTH: 15
91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
93 <220> FEATURE:
94 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 52-66
97 <400> SEQUENCE: 6
98 Gln Asp Leu Thr Val Met Ala Ala Leu Gly Leu Gly Phe Leu Thr
E--> 99 1 5 10 15
103 <210> SEQ ID NO: 7
104 <211> LENGTH: 15
105 <212> TYPE: PRT
106 <213> ORGANISM: Homo sapiens
108 <220> FEATURE:
109 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 62-76
111 <400> SEQUENCE: 7
112 Leu Gly Phe Leu Thr Ser Asn Phe Arg Arg His Ser Trp Ser Ser
E--> 113 1 5 10 15
117 <210> SEQ ID NO: 8
118 <211> LENGTH: 15
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
122 <220> FEATURE:
123 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 72-86
125 <400> SEQUENCE: 8
126 His Ser Trp Ser Ser Val Ala Phe Asn Leu Phe Met Leu Ala Leu
E--> 127 1 5 10 15
131 <210> SEQ ID NO: 9
132 <211> LENGTH: 15
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <220> FEATURE:
137 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 82-96

p.3

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,097A

DATE: 09/19/2002

TIME: 13:04:24

Input Set : A:\EP.txt

Output Set: N:\CRF4\09192002\I857097A.raw

139 <400> SEQUENCE: 9
140 Phe Met Leu Ala Leu Gly Val Gln Trp Ala Ile Leu Leu Asp Gly *same* 15
E--> 141 1 5 10
146 <210> SEQ ID NO: 10
147 <211> LENGTH: 15
148 <212> TYPE: PRT
149 <213> ORGANISM: Homo sapiens
151 <220> FEATURE:
152 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 92-106
154 <400> SEQUENCE: 10
155 Ile Leu Leu Asp Gly Phe Leu Ser Gln Phe Pro Pro Gly Lys Val *same* 15
E--> 156 1 5 10
160 <210> SEQ ID NO: 11
161 <211> LENGTH: 15
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <220> FEATURE:
166 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 102-116
168 <400> SEQUENCE: 11
169 Pro Pro Gly Lys Val Val Ile Thr Leu Phe Ser Ile Arg Leu Ala *same* 15
E--> 170 1 5 10
174 <210> SEQ ID NO: 12
175 <211> LENGTH: 15
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <220> FEATURE:
180 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 112-126
182 <400> SEQUENCE: 12
183 Ser Ile Arg Leu Ala Thr Met Ser Ala Met Ser Val Leu Ile Ser *same* 15
E--> 184 1 5 10
185 <210> SEQ ID NO: 13
186 <211> LENGTH: 15
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <220> FEATURE:
193 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 122-136
195 <400> SEQUENCE: 13
196 Ser Val Leu Ile Ser Ala Gly Ala Val Leu Gly Lys Val Asn Leu *same* 15
E--> 197 1 5 10
201 <210> SEQ ID NO: 14
202 <211> LENGTH: 15
203 <212> TYPE: PRT
204 <213> ORGANISM: Homo sapiens
206 <220> FEATURE:
207 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 132-146 *same*
209 <400> SEQUENCE: 14
210 Gly Lys Val Asn Leu Ala Gln Leu Val Val Met Val Leu Val Glu
E--> 211 1 5 10 15
215 <210> SEQ ID NO: 15

p.4

RAW SEQUENCE LISTING

DATE: 09/19/2002

PATENT APPLICATION: US/09/857,097A

TIME: 13:04:24

Input Set : A:\EP.txt

Output Set: N:\CRF4\09192002\I857097A.raw

216 <211> LENGTH: 15
217 <212> TYPE: PRT
218 <213> ORGANISM: Homo sapiens
220 <220> FEATURE:
221 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 142-156
223 <400> SEQUENCE: 15
224 Met Val Leu Val Glu Val Thr Ala Leu Gly Thr Leu Arg Met Val *same*
E--> 225 1 5 10 15
229 <210> SEQ ID NO: 16
230 <211> LENGTH: 15
231 <212> TYPE: PRT
232 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
235 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 152-166
241 <400> SEQUENCE: 16
242 Thr Leu Arg Met Val Ile Ser Asn Ile Phe Asn Thr Asp Tyr His *same*
E--> 243 1 5 10 15
247 <210> SEQ ID NO: 17
248 <211> LENGTH: 15
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
252 <220> FEATURE:
253 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 162-176
255 <400> SEQUENCE: 17
256 Asn Thr Asp Tyr His Met Asn Leu Arg His Phe Tyr Val Phe Ala *same*
E--> 257 1 5 10 15
261 <210> SEQ ID NO: 18
262 <211> LENGTH: 15
263 <212> TYPE: PRT
264 <213> ORGANISM: Homo sapiens
266 <220> FEATURE:
267 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 172-186
269 <400> SEQUENCE: 18
270 Phe Tyr Val Phe Ala Ala Tyr Phe Gly Leu Thr Val Ala Trp Cys *same*
E--> 271 1 5 10 15
275 <210> SEQ ID NO: 19
276 <211> LENGTH: 15
277 <212> TYPE: PRT
278 <213> ORGANISM: Homo sapiens
281 <220> FEATURE:
282 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 182-196
284 <400> SEQUENCE: 19
285 Thr Val Ala Trp Cys Leu Pro Lys Pro Leu Pro Lys Gly Thr Glu *same*
E--> 286 1 5 10 15
291 <210> SEQ ID NO: 20
292 <211> LENGTH: 15
293 <212> TYPE: PRT
294 <213> ORGANISM: Homo sapiens
296 <220> FEATURE:

P.S

RAW SEQUENCE LISTING

DATE: 09/19/2002

PATENT APPLICATION: US/09/857,097A

TIME: 13:04:24

Input Set : A:\EP.txt

Output Set: N:\CRF4\09192002\I857097A.raw

297 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 192-206

299 <400> SEQUENCE: 20

300 Pro Lys Gly Thr Glu Asp Asn Asp Gln Arg Ala Thr Ile Pro Ser

E--> 301 1

5

10

15

IMPORTANT

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

see p. 6 for more errors

09/857,097A

6

<210> 46 ← last sequence in submitted file
<211> 15
<212> PRT
<213> Homo sapiens

<220>

<223> RhCE (R1 Ce) Residue 222-236

where are amino acids?

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/857,097A

DATE: 09/19/2002
TIME: 13:04:25

Input Set : A:\EP.txt
Output Set: N:\CRF4\09192002\I857097A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 31
Seq#:4; Line(s) 72
Seq#:6; Line(s) 99
Seq#:7; Line(s) 113
Seq#:8; Line(s) 127
Seq#:9; Line(s) 141
Seq#:14; Line(s) 211
Seq#:15; Line(s) 225
Seq#:17; Line(s) 257
Seq#:18; Line(s) 271
Seq#:22; Line(s) 328
Seq#:24; Line(s) 356
Seq#:36; Line(s) 524
Seq#:39; Line(s) 565
Seq#:41; Line(s) 595
Seq#:42; Line(s) 609
Seq#:43; Line(s) 627
Seq#:44; Line(s) 641
Seq#:45; Line(s) 656

VERIFICATION SUMMARY

DATE: 09/19/2002

PATENT APPLICATION: US/09/857,097A

TIME: 13:04:25

Input Set : A:\EP.txt

Output Set: N:\CRF4\09192002\I857097A.raw

L:31 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:45 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:58 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:72 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:86 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:93 M:283 W: Missing Blank Line separator, <220> field identifier
L:99 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:113 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:127 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:141 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:156 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:170 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
L:184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
L:197 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
L:211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:225 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
L:243 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:257 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:271 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
L:286 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19
L:301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
L:315 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:328 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:342 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:356 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
L:369 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:25
L:380 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
L:395 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28
L:422 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
L:438 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:30
L:452 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:467 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:483 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:33
L:497 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34
L:511 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:524 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:539 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
L:553 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:565 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:581 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:595 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
L:627 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:641 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:656 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:17 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (152) Counted (45)